



SEQUENCE LISTING

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Bate, Nicholas

<120> A Repressor-Mediated Regulation System for Control of Gene Expression
in Plants

<130> 1096.021A

<140> US 10/719,996

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<150> PCT/CA02/00740

<151> 2002-05-23

<150> US 60/292,973

<151> 2001-05-23

<160> 44

<170> PatentIn version 3.0

<210> 1

<211> 429

<212> DNA

<213> Agrobacterium tumefaciens

<400> 1
atgacggaaa ctgcatacgg taacgcccag gatctgctgg tcgaactgac ggcggatatt 60
gtggctgcct atgtagcaa ccacgtcggt ccggtaactg agcttcccgg cttatttcg 120
gatgttcata cggcactcag cggaacatcg gcaccggcat cggtggcggg caatgttgaa 180
aagcagaagc ctgctgtgtc gggtcgcaag tcgggttcagg acgatcatat cgtctgtttg 240
gaatgtgggtg gctcgttcaa gtcgctcaaa cgccacctga cgacgcata cagcatgacg 300
ccggaagaat atcgcgaaaa atgggatctg ccgggtcgatt atccgatggt tgctcccgcc 360
tatgccgaag cccgttcgcg gctcgccaag gaaatgggtc tcggtcagcg ccgcaaggcg 420

aaccgttga

429

<210> 2

<211> 458

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic ROS optimized for plant codon usage and encoding fusion
of ROS and nuclear localization signal

<400> 2

atgactgaga ctgcttacgg taacgctcag gatcttcttg ttgagcttac tgctgatatc	60
gttgctgctt acgtttctaa ccacgttggt cctgttactg agcttcctgg acttatctct	120
gatgttcata ctgcactttc tggaacatct gctcctgctt ctggtgctgt taacgttgag	180
aagcagaagc ctgctgtttc tggtcgtaag tctgttcagg atgatcatat cgtttgtttg	240
gagtgtggtg gttctttcaa gtctctcaag cgtcacctta ctactcatca ctctatgact	300
ccagaggagt atagagagaa gtgggatctt cctgttgatt accctatggg tgctcctgct	360
tacgctgagg ctcggttctcg tctcgctaag gagatgggtc tcggtcagcg tcgtaaggct	420
aaccgtccaa aaaagaagcg taaggtctga gagctcgc	458

<210> 3

<211> 447

<212> DNA

<213> Artificial sequence

<220>

<223> ROS consensus sequence

<220>

<221> misc_feature

<222> (1)..(447)

<223> n is A or T or G or C

<220>

<221> misc_feature

<222> (1)..(447)

<223> h is a or c or t/u

<220>

<221> misc_feature

<222> (1)..(447)

<223> m is a or c

<220>

<221> misc_feature

<222> (1)..(447)

<223> r is G or A

<220>

<221> misc_feature

<222> (1)..(447)

<223> y is t/u or c

<220>

<221> misc_feature

<222> (1)..(447)

<223> w is a or t/u

<400> 3

atgacngara cngentaygg naaygncar gayytnytng tngarytnac ngcngayath 60

gtngcngcnt aygtwnsnaa ycaygtngtn ccngtnacng arytnccngg nytnathwsn 120

gaygtncaya cngcnytnws nggnacnwsn gncncngcnw sngtngcngt naaygtngar 180

aarcaraarc cngcngtnws ngtnmgnaar wsngtncarg aygaycayat hgtntgyytn 240

gartgyggng gnwsnttyaa rwsnytnaar mgncayytna cnacncayca ywsnatgacn 300

ccngargart aymngaraa rtgggayytn ccngtngayt ayccnatggt ngcncngcn	360
taygcngarg cnmgnwsnmg nytngcnaar garatgggny tnggncarmg nmгнаaargcn	420
aaymgncna araaraarmg naargtn	447

<210> 4

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> sense primer for amplifying ROS coding region

<400> 4	
gcggatccga tgacggaaac tgcatac	27

<210> 5

<211> 25

<212> DNA

<213> Artificial sequence

<220>

<223> antisense primer for amplifying ROS coding region

<400> 5	
gcaagcttca acggttcgcc ttgcg	25

<210> 6

<211> 36

<212> DNA

<213> Artificial

<220>

<223> sense primer for amplifying tms2 promoter

<400> 6
 tgcggatgca taagcttgct gacattgcta gaaaag 36

<210> 7
 <211> 26
 <212> DNA
 <213> Artificial sequence

<220>
 <223> antisense primer for amplifying tms2 promoter

<400> 7
 cggggatcct ttcagggcca tttcag 26

<210> 8
 <211> 25
 <212> DNA
 <213> Artificial sequence

<220>
 <223> ROS operator sequence

<400> 8
 tatatttcaa ttttattgta atata 25

<210> 9
 <211> 109
 <212> DNA
 <213> Artificial sequence

<220>
 <223> ROS-OPDS oligo for p74-315 construct

<400> 9
 atctccactg acgtaaggga tgacgcacaa tcccactatc cttcgcaaga cccttctct 60
 atataatata tttcaatttt attgtaatat aacacggggg actctagag 109

<210> 10

<211> 113
 <212> DNA
 <213> Artificial sequence

<220>
 <223> ROS-OPDA oligo for p74-315 construct

<400> 10
 gatcctctag agtcccccggt gttatattac aataaaattg aaatatatta tatagaggaa 60
 gggctcttgcg aaggatagtg ggattgtgcg tcatccotta cgtcagtgga gat 113

<210> 11
 <211> 107
 <212> DNA
 <213> Artificial sequence

<220>
 <223> ROS-OPUS oligo for p74-316 construct

<400> 11
 atctccactg acgtaaggga tgacgcacaa tctatatttc aattttattg taatatacta 60
 tataagggaag ttcatttcat ttggagagaa cacgggggac tctagag 107

<210> 12
 <211> 111
 <212> DNA
 <213> Artificial sequence

<220>
 <223> ROS-OPUA oligo for p74-316 construct

<400> 12
 gatcctctag agtcccccggt gttctctcca aatgaaatga acttccttat atagtatatt 60
 acaataaaat tgaaatatag attgtgcgctc atcccttacg tcagtggaga t 111

<210> 13

<211> 108

<212> DNA

<213> Artificial sequence

<220>

<223> ROS-OPPS oligo for p74-309 construct

<400> 13

atctccactg acgtaaggga tgacgcacaa tctatatattc aattttattg taatatacta 60

tataatatat ttcaatttta ttgtaatata acacggggga ctctagag 108

<210> 14

<211> 112

<212> DNA

<213> Artificial sequence

<220>

<223> ROS-OPPA oligo for p74-309 construct

<400> 14

gacccctctag agtcccccggt gttatattac aataaaattg aaatatatta tatagtatat 60

tacaataaaa ttgaaatata gattgtgcgt catcccttac gtcagtggag at 112

<210> 15

<211> 59

<212> DNA

<213> Artificial sequence

<220>

<223> ROS-OP1 oligo for p76-508 construct

<400> 15

gacccctatat ttcaatttta ttgtaatata gctatatattc aattttattg taatataat 59

<210> 16

<211> 57

<212> DNA

<213> Artificial sequence

<220>

<223> ROS-OP2 oligo for p76-508 construct

<400> 16

cgattatatt acaataaaat tgaaatatag ctatattaca ataaaattga aatatag 57

<210> 17

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> sense primer for amplifying Actin2 promoter

<400> 17

aagcttatgt atgcaagagt cagc 24

<210> 18

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> antisense primer for amplifying Actin2 promoter

<400> 18

ttgactagta tcagcctcag ccat 24

<210> 19

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> ROS operator sequence in ipt gene

<400> 19

tataattaata atattaactg tcgcatt

27

<210> 20

<211> 10

<212> DNA

<213> Artificial sequence

<220>

<223> consensus ROS operator sequence

<400> 20

watdhwkmar

10

<210> 21

<211> 104

<212> PRT

<213> Agrobacterium radiobacter

<400> 21

Met Thr Thr Ala Tyr Gly Asn Ala Asp Val Thr Ala Asp Val Ala Ala
1 5 10 15

Tyr Val Ser Asn His Val Val Val Thr Gly Ser Asp Val His Thr Ala
20 25 30

Ser Gly Thr Ser Ala Ala Ser Val Ala Val Asn Val Lys Lys Ala Val
35 40 45

Ser Val Arg Lys Ser Val Asp Asp His Val Cys Cys Gly Gly Ser Lys
50 55 60

Ser Lys Arg His Thr Thr His His Ser Met Thr Tyr Arg Lys Trp Asp
65 70 75 80

Val Asp Tyr Met Val Ala Ala Tyr Ala Ala Arg Ser Arg Ala Lys Met
85 90 95

Gly Gly Arg Arg Lys Ala Asn Arg
100

<210> 22

<211> 138

<212> DNA

<213> Artificial sequence

<220>

<223> p74-315 sequence from EcoRV site to ATG codon of GUS

<400> 22

gatatctcca ctgacgtaag ggatgacgca caatcccact atccttcgca agacccttcc 60

tctatataat atatttcaat tttattgtaa tataacacgg gggactctag aggatccccg 120

ggtggtcagt cccttatg 138

<210> 23

<211> 136

<212> DNA

<213> Artificial sequence

<220>

<223> p74-316 sequence from EcoRV site to ATG codon of GUS

<400> 23

gatatctcca ctgacgtaag ggatgacgca caatctatat ttcaatttta ttgtaatata 60

ctatataagg aagttcattt catttggaga gaacacgggg gactctagag gatccccggg 120

tggtcagtcc cttatg 136

<210> 24

<211> 137

<212> DNA

<213> Artificial sequence

<220>

<223> p74-309 sequence from EcoRV site to ATG codon of GUS

<400> 24

gatatctcca ctgacgtaag ggatgacgca caatctatat ttcaatttta ttgtaatata 60

ctatataata tatttcaatt ttattgtaat ataacacggg ggactctaga ggatccccgg 120

gtggtcagtc ccttatg 137

<210> 25
 <211> 237
 <212> DNA
 <213> Artificial sequence

<220>
 <223> p74-118 sequence from EcoRV site to ATG codon of GUS

<400> 25
 gatattctcca ctgacgtaag ggatgacgca caatcccact atccttcgca agacccttcc 60
 tctatataat atatttcaat tttattgtaa tataacacgg gggactctag aggatcctat 120
 atttcaattt tattgtaata tagctatatt tcaattttat tgtaatataa tcgatttcga 180
 acccggggga ccgaattcct cgagtctaga ggatccccgg gtggtcagtc ccttatg 237

<210> 26
 <211> 142
 <212> PRT
 <213> Agrobacterium tumefaciens

<400> 26
 Met Thr Glu Thr Ala Tyr Gly Asn Ala Gln Asp Leu Leu Val Glu Leu
 1 5 10 15
 Thr Ala Asp Ile Val Ala Ala Tyr Val Ser Asn His Val Val Pro Val
 20 25 30
 Thr Glu Leu Pro Gly Leu Ile Ser Asp Val His Thr Ala Leu Ser Gly
 35 40 45
 Thr Ser Ala Pro Ala Ser Val Ala Val Asn Val Glu Lys Gln Lys Pro
 50 55 60
 Ala Val Ser Val Arg Lys Ser Val Gln Asp Asp His Ile Val Cys Leu
 65 70 75 80
 Glu Cys Gly Gly Ser Phe Lys Ser Leu Lys Arg His Leu Thr Thr His
 85 90 95
 His Ser Met Thr Pro Glu Glu Tyr Arg Glu Lys Trp Asp Leu Pro Val
 100 105 110
 Asp Tyr Pro Met Val Ala Pro Ala Tyr Ala Glu Ala Arg Ser Arg Leu
 115 120 125

Ala Lys Glu Met Gly Leu Gly Gln Arg Arg Lys Ala Asn Arg
 130 135 140

<210> 27

<211> 149

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic-ROS fused to nuclear localization signal

<400> 27

Met Thr Glu Thr Ala Tyr Gly Asn Ala Gln Asp Leu Leu Val Glu Leu
 1 5 10 15

Thr Ala Asp Ile Val Ala Ala Tyr Val Ser Asn His Val Val Pro Val
 20 25 30

Thr Glu Leu Pro Gly Leu Ile Ser Asp Val His Thr Ala Leu Ser Gly
 35 40 45

Thr Ser Ala Pro Ala Ser Val Ala Val Asn Val Glu Lys Gln Lys Pro
 50 55 60

Ala Val Ser Val Arg Lys Ser Val Gln Asp Asp His Ile Val Cys Leu
 65 70 75 80

Glu Cys Gly Gly Ser Phe Lys Ser Leu Lys Arg His Leu Thr Thr His
 85 90 95

His Ser Met Thr Pro Glu Glu Tyr Arg Glu Lys Trp Asp Leu Pro Val
 100 105 110

Asp Tyr Pro Met Val Ala Pro Ala Tyr Ala Glu Ala Arg Ser Arg Leu
 115 120 125

Ala Lys Glu Met Gly Leu Gly Gln Arg Arg Lys Ala Asn Arg Pro Lys
 130 135 140

Lys Lys Arg Lys Val
 145

<210> 28

<211> 143

<212> PRT

<213> rhizobium elti

<400> 28

Met	Thr	Asp	Met	Ala	Thr	Gly	Asn	Ala	Pro	Glu	Leu	Leu	Val	Glu	Leu	1	5	10	15
Thr	Ala	Asp	Ile	Val	Ala	Ala	Tyr	Val	Ser	Asn	His	Val	Val	Pro	Val	20	25	30	
Ser	Asp	Leu	Ala	Asn	Leu	Ile	Ser	Asp	Val	His	Ser	Ala	Leu	Ser	Asn	35	40	45	
Thr	Ser	Val	Pro	Gln	Pro	Ala	Ala	Ala	Val	Val	Glu	Lys	Gln	Lys	Pro	50	55	60	
Ala	Val	Ser	Val	Arg	Lys	Ser	Val	Gln	Asp	Glu	Gln	Ile	Thr	Cys	Leu	65	70	75	80
Glu	Cys	Gly	Gly	Asn	Phe	Lys	Ser	Leu	Lys	Arg	His	Leu	Met	Thr	His	85	90	95	
His	Ser	Leu	Ser	Pro	Glu	Glu	Tyr	Arg	Glu	Lys	Trp	Asp	Leu	Pro	Thr	100	105	110	
Asp	Tyr	Pro	Met	Val	Ala	Pro	Ala	Tyr	Ala	Glu	Ala	Arg	Ser	Arg	Leu	115	120	125	
Ala	Lys	Glu	Met	Gly	Leu	Gly	Gln	Arg	Arg	Lys	Arg	Gly	Arg	Gly	130	135	140		

<210> 29

<211> 142

<212> PRT

<213> agrobacterium radiobacter

<400> 29

Met	Thr	Glu	Thr	Ala	Tyr	Gly	Asn	Ala	Gln	Asp	Leu	Leu	Val	Glu	Leu	1	5	10	15
Thr	Ala	Asp	Ile	Val	Ala	Ala	Tyr	Val	Ser	Asn	His	Val	Val	Pro	Val	20	25	30	
Thr	Glu	Leu	Pro	Gly	Leu	Ile	Ser	Asp	Val	His	Thr	Ala	Leu	Ser	Gly	35	40	45	
Thr	Ser	Ala	Pro	Ala	Ser	Val	Ala	Val	Asn	Val	Glu	Lys	Gln	Lys	Pro	50	55	60	
Ala	Val	Ser	Val	Arg	Lys	Ser	Val	Gln	Asp	Asp	His	Ile	Val	Cys	Leu	65	70	75	80
Glu	Cys	Gly	Gly	Ser	Phe	Lys	Ser	Leu	Lys	Arg	His	Leu	Thr	Thr	His	85	90	95	
His	Ser	Met	Thr	Pro	Glu	Glu	Tyr	Arg	Glu	Lys	Trp	Asp	Leu	Gln	Val	100	105	110	
Asp	Tyr	Pro	Met	Val	Ala	Pro	Ala	Tyr	Ala	Glu	Ala	Arg	Ser	Arg	Leu				

115	120	125
Ala Lys Glu Met Gly Leu Gly Gln Arg Arg Lys Ala Asn Arg		
130	135	140

<210> 30

<211> 143

<212> PRT

<213> rhizobium meliloti

<400> 30

Met Thr Glu Thr Ser Leu Gly Thr Ser Asn Glu Leu Leu Val Glu Leu
1 5 10 15
Thr Ala Glu Ile Val Ala Ala Tyr Val Ser Asn His Val Val Pro Val
20 25 30
Ala Glu Leu Pro Thr Leu Ile Ala Asp Val His Ser Ala Leu Asn Asn
35 40 45
Thr Thr Ala Pro Ala Pro Val Val Val Pro Val Glu Lys Pro Lys Pro
50 55 60
Ala Val Ser Val Arg Lys Ser Val Gln Asp Asp Gln Ile Thr Cys Leu
65 70 75 80
Glu Cys Gly Gly Thr Phe Lys Ser Leu Lys Arg His Leu Met Thr His
85 90 95
His Asn Leu Ser Pro Glu Glu Tyr Arg Asp Lys Trp Asp Leu Pro Ala
100 105 110
Asp Tyr Pro Met Val Ala Pro Ala Tyr Ala Glu Ala Arg Ser Arg Leu
115 120 125
Ala Lys Glu Met Gly Leu Gly Gln Arg Arg Lys Arg Arg Gly Lys
130 135 140

<210> 31

<211> 16

<212> PRT

<213> Arabidopsis sp.

<400> 31

Arg Ile Glu Asn Thr Thr Asn Arg Gln Val Thr Phe Cys Lys Arg Arg
1 5 10 15

<210> 32

<211> 18

<212> PRT

<213> Nicotiana sp.

<400> 32

Arg Arg Leu Ala Gln Asn Arg Glu Ala Ala Arg Lys Ser Arg Leu Arg
1 5 10 15

Lys Lys

<210> 33

<211> 21

<212> PRT

<213> Nicotiana sp.

<400> 33

Lys Lys Arg Ala Arg Leu Val Arg Asn Arg Glu Ser Ala Gln Leu Ser
1 5 10 15

Arg Gln Arg Lys Lys
20

<210> 34

<211> 18

<212> PRT

<213> Zea mays

<400> 34

Arg Lys Arg Lys Glu Ser Asn Arg Glu Ser Ala Arg Arg Ser Arg Tyr
1 5 10 15

Arg Lys

<210> 35

<211> 47

<212> PRT

<213> Unknown

<220>

<223> potyvirus nuclear localization signal

<220>

<221> misc_feature

<222> (12)..(44)

<223> unknown or other amino acid

<400> 35

Lys	Lys	Asn	Gln	Lys	His	Lys	Leu	Lys	Ala	Ala	Met	Xaa	Xaa	Xaa	Xaa
1				5					10					15	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20					25					30		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Lys	Arg	Lys	
			35				40					45			

<210> 36

<211> 17

<212> PRT

<213> Xenopus sp.

<400> 36

Lys	Arg	Pro	Ala	Ala	Thr	Lys	Lys	Ala	Gly	Gln	Ala	Lys	Lys	Lys	Lys
1				5					10					15	
Leu															

<210> 37

<211> 17

<212> PRT

<213> Xenopus sp.

<400> 37

Lys	Arg	Ile	Ala	Pro	Asp	Ser	Ala	Ser	Lys	Val	Pro	Arg	Lys	Lys	Thr
1				5					10					15	
Arg															

<210> 38

<211> 17

<212> PRT

<213> *Xenopus* sp.

<400> 38

Lys	Arg	Lys	Thr	Glu	Glu	Glu	Ser	Pro	Leu	Lys	Asp	Lys	Asp	Ala	Lys
1				5					10					15	

Lys

<210> 39

<211> 17

<212> PRT

<213> *Mus* sp./*Rattus* sp.

<400> 39

Arg	Lys	Cys	Leu	Gln	Ala	Gly	Met	Asn	Leu	Glu	Ala	Arg	Lys	Thr	Lys
1				5					10					15	

Lys

<210> 40

<211> 17

<212> PRT

<213> *Homo sapiens*

<400> 40

Arg	Lys	Cys	Leu	Gln	Ala	Gly	Met	Asn	Leu	Glu	Ala	Arg	Lys	Thr	Lys
1				5					10					15	

Lys

<210> 41

<211> 17

<212> PRT

<213> Homo sapiens

<400> 41

Arg Lys Cys Leu Gln Ala Gly Met Asn Leu Glu Ala Arg Lys Thr Lys
1 5 10 15

Lys

<210> 42

<211> 17

<212> PRT

<213> Gallus sp.

<400> 42

Arg Lys Cys Cys Gln Ala Gly Met Val Leu Gly Gly Arg Lys Phe Lys
1 5 10 15

Lys

<210> 43

<211> 17

<212> PRT

<213> Homo sapiens

<400> 43

Arg Lys Cys Tyr Glu Ala Gly Met Thr Leu Gly Ala Arg Lys Leu Lys
1 5 10 15

Lys

<210> 44

<211> 17

<212> PRT

<213> Gallus sp.

<400> 44

Arg	Arg	Cys	Phe	Glu	Val	Arg	Val	Cys	Ala	Cys	Pro	Gly	Arg	Asp	Arg
1				5					10					15	

Lys